



09,883,118.

Cole \$

PATENT
Customer No. 22,852
Attorney Docket No. 6832.0017

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re U.S. Patent No.: 6,905,688)
Inventors:)
Craig A. Rosen and William A. Haseltine)
Issue Date.: June 14, 2005)
For: ALBUMIN FUSION PROTEINS)

Certificate
MAR 09 2006
of Correction

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

03/08/2006 SZENDIEI 0000067 6905608

01 FC:1611

100.00 OP

Sir:

REQUEST FOR CERTIFICATE OF CORRECTION

Pursuant to 35 U.S.C. §§ 254 and 255, and 37 C.F.R. §§ 1.322 and 1.323, this is a request for a Certificate of Correction in the above-identified patent. Some of the mistakes identified in the appended Form occurred through the fault of the Patent Office, as clearly disclosed by the records of the application which matured into this patent.

For example, the priority claims to Provisional Application Nos. 60/256,931, filed December 21, 2000; 60/199,384, filed April 25, 2000; and 60/229,358, filed April 12, 2000, were deleted in an Amendment filed June 3, 2004, and a Corrected Filing Receipt reflecting the change was mailed by the PTO on June 21, 2004. However, the issued patent was printed with the priority claims in the title page under item (60) and in the first paragraph of the specification.

03/08/2006 SZENDIEI 0000067 6905608

01 FC:1611

100.00 OP

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Moreover, the issued patent reflects the original Sequence Listing filed rather than the Substitute Sequence Listing submitted on May 12, 2004. The Sequence Listing in the attached Certificate of Correction is identical to the Substitute Sequence Listing filed on May 12, 2004, and is also identical to the computer readable copy of the Substitute Sequence Listing also submitted on May 18, 2004. Thus, the correction contains no new matter.

Finally, the issued patent contains an error in the claims due to an Office mistake. The issued claims are based on an Examiner's Amendment mailed with a Notice of Allowance dated February 12, 2004. Claim 4 recited "in vivo biological activity" in the Examiner's Amendment but the patent issued as "in viva biological activity." The Certificate of Correction corrects this typographical error.

Other mistakes identified in the appended Form are of a clerical or typographical nature, or of minor character, and resulted from an error made in good faith by Patentees by failing to bring to the attention of the Examiner the clerical/typographical errors in the claims presented in the Examiner's Amendment of February 12, 2004.

A check in the amount of \$100 (the fee set forth in 37 C.F.R. § 1.20(a)) is attached. Should a check not be appended or should any additional fees be needed, authorization is hereby given to charge any fees due in connection with the filing of this request to Deposit Account No. 06-0916.

Two (2) copies of PTO Form 1050 are appended. The complete Certificate of Correction involves twenty-seven (27) pages. Issuance of the Certificate of Correction containing the correction is earnestly requested.

Please charge any required fees not included herewith to our deposit account
06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,
GARRETT & DUNNER, L.L.P.

Dated: March 7, 2006

By: Charles E. Van Horn
Charles E. Van Horn
Reg. No. 40,266

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. 6,905,688
APPLICATION NO.: 09/833,118
ISSUE DATE: June 14, 2005
INVENTOR(S): Craig A. Rosen et al.

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Title Page

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending "provisional application No. 60/199,384, filed on Apr. 25, 2000."

In the Specification:

Col. 1, line 3, delete the text beginning with "This application" to and ending "in its entirety." in col. 1, line 8.

In the Claims:

Col. 292, lines 36-37, in claim 1(j), delete the text "wherein the brain derived neurotrophic factor protein or fragment thereof,".

Col. 292, line 57, in claim 4, "viva" should read --vivo--.

Col. 294, line 15, in claim 15, delete "any of".

Col. 294, line 17, in claim 16, delete "any of".

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, beginning with the text "<160> NUMBER OF SEQ ID NOS: 35" to and ending "<400> SEQUENCE: 35

Met	Pro	Thr	Trp	Ala	Trp	Trp	Leu	Phe	Leu	Val	Leu	Leu	Leu	Ala	Leu
1					5				10					15	

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U.S. Patent No. 6,905,688

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Garrett & Dunner, L.L.P.
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Trp Ala Pro Ala Arg Gly"

20

in Col. 292 and insert the following Sequence Listing:

<160> NUMBER OF SEQ ID NOS: 45

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer useful to clone human growth hormone cDNA

<400> 1

cccaagaatt cccttatcca ggc

23

<210> 2

<211> 33

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<213> Artificial Sequence

<220>

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<223> primer useful to clone human growth hormone cDNA

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gggaagctta gaagccacag gatccctcca cag

33

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<211> 16

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<213> Artificial Sequence

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<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 3

gataaagatt cccaac

16

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

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<400> 4
aattgttggg aatcttt

17

<210> 5
<211> 17
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with non-cohesive ends.

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17

<210> 6
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aattgttggg aataagcc

18

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<223> invertase leader sequence

<220>
<221> SITE
<222> 20)..(24)
<223> first 5 amino acids of mature human serum albumin

<400> 7
Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser
20

<210> 8
<211> 21

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<212> DNA
<213> Artificial Sequence

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<221> misc_structure
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fragments with non-cohesive ends.

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fragments with non-cohesive ends.

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<213> Artificial Sequence

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<211> 30
<212> DNA
<213> Artificial Sequence

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<210> 12
<211> 31
<212> DNA

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<213> Artificial Sequence

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<213> Artificial Sequence

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<211> 48
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<400> 14
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<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

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ac 62

<210> 16
<211> 63
<212> DNA

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<213> Artificial Sequence

<220>

<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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gcc 63

<210> 17

<211> 1782

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1755)

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1 5 10 15

gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

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130	135	140	
aga cat cct tac ttt tat gcc cgc gaa ctc ctt ttc ttt gct aaa agg			480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Phe Phe Ala Lys Arg			
145	150	155	160
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc			528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
165	170	175	
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg			576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
180	185	190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa			624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
195	200	205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc			672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
210	215	220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa			720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
225	230	235	240
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac			768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
245	250	255	
agg cgc gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc			816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
260	265	270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac			864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
275	280	285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca			912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
290	295	300	
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct			960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
305	310	315	320
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga			1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg			
325	330	335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca			1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr			
340	345	350	
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa			1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu			
355	360	365	

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
370 375 380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	
545 550 555 560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt	1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val	
565 570 575	
gct gca agt caa gct gcc tta gcc tta taacatctac atttaaaagc atctcag	1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu	
580 585	

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<210> 18
 <211> 585
 <212> PRT
 <213> Homo Sapiens

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 20 25 30
 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110
 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125
 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140
 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160
 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240
 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255
 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

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Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

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Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 19
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
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<223> primer used to generate XhoI and ClaI
site in pPPC0006

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<210> 20
<211> 59
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site in pPPC0006

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site in pPPC0006

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<400> 22
cacttctcta gagtggttc atatgtctt

29

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sites in pPPC0007

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<223> forward primer useful for generation of albumin
fusion protein in which the albumin moiety is N-terminal
of the Therapeutic Protein

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

9 2006


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<212> DNA
<213> Artificial Sequence

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of the Therapeutic Protein

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Washington, D.C. 20001-4413

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MAILING ADDRESS OF SENDER

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Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

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U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

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<210> 29
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<213> Artificial Sequence

<220>
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<223> signal peptide of natural human serum albumin protein

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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
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901 New York Avenue, N.W.
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```

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Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
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Washington, D.C. 20001-4413

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<223> reverse complement of stop codon

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<223> AscI restriction site

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<223> reverse complement of DNA sequence encoding last 9 amino acids

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<210> 32
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<223> forward primer useful for inserting Therapeutic
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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
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901 New York Avenue, N.W.
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MAR 9 2006

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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

MAR 9 2006


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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

MAR 9 2000

<223> n equals a,t,g, or c

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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

MAR 9 2000

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<211> 17
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<213> Artificial Sequence

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1             5             10            15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

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Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Ala Leu
1             5             10            15

Trp Ala Pro Ala Arg Gly
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<213> Homo sapiens

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aattcgaggg tgcaccgtca gtcttctctt tcccccaaaa acccaaggac accctcatga    120
tctcccgagc tcttgaggtc acatgcgtgg tgggtggactg aagccacgaa gacctgagg      180
tcaagttcaa ctggtactgt gacggcgctgg aggtgcataa tgccaagaca aagccgcggg      240

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U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
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MAR 9 2008

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aggagcagta caacagcacg tacctgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
agaaaacct ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgectggtc aaagcttct 480
atccaagcga catcgccgtg gaggggaga gcaatggga gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ccttcttct ctacagcaag ctcaccgttg 600
acaagagcag gtggcagcag gggaaactct tctcatgctc cgtgatgcat gaggtcttgc 660
acaaccacta cgcgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733

<210> 37
<211> 5
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<220>
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<400> 37
Trp Ser Xaa Trp Ser
1 5

<210> 38
<211> 86
<212> DNA
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<223> forward primer useful for generation of a synthetic gamma activation site
(GAS) containing promoter element

<400> 38
gcgcctcgag atttccccc aatctagatt tccccgaaat gatttccccg aaatgatttc 60
cccgaaatat ctgccatctc aattag 86

<210> 39
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<213> Artificial Sequence

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(GAS) containing promoter element

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gcggcaagct tttgcaaag cctaggg                27

<210> 40
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 40
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg        60
aatatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgccccatccc      120
gcccttaact cgcgccagtt ccgcccattc tcgcgcccat ggctgactaa ttttttttat      180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt      240
ttttggaggc ctaggctttt gcaaaaagct t                                271

<210> 41
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<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 41
gcgctcgagg gatgacagcg atagaacccc gg                                32

<210> 42
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<212> DNA
<213> Artificial Sequence

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<223> primer useful for generation of a EGR/SEAP reporter construct

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gcgaagcttc gcgaactccc ggatccgcct c                                31

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<213> Artificial Sequence

<220>
<221> misc_binding
<223> NF-KB binding site

<400> 43
ggggacttcc cc                                12

<210> 44
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
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<223> forward primer useful for generation of a vector containing the NF-KB
promoter element

<400> 44
gcggcctcga ggggacttcc cgggggactt tccggggact ttccgggact ttccatcctg  60

ccatctcaat tag                                73

<210> 45
<211> 256
<212> DNA
<213> Artificial Sequence

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<221> misc_feature
<223> Synthetic NF-KB/SV40 promoter

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ctcgagggga ctttcccggg gactttccgg ggactttccg ggaatttcca tctgccatct  60

caattagtea gcaaccatag tcccgccctt aactccgcc atcccgcccc taactccgcc  120

cagttccgcc cattctccgc cccatggctg actaattttt ttattttatg cagaggccga  180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg  240

cttttgcaaa aagctt                                256

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Washington, D.C. 20001-4413

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. 6,905,688
APPLICATION NO.: 09/833,118
ISSUE DATE: June 14, 2005
INVENTOR(S): Craig A. Rosen et al.

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Title Page

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending "provisional application No. 60/199,384, filed on Apr. 25, 2000."

In the Specification:

Col. 1, line 3, delete the text beginning with "This application" to and ending "in its entirety." in col. 1, line 8.

In the Claims:

Col. 292, lines 36-37, in claim 1(j), delete the text "wherein the brain derived neurotrophic factor protein or fragment thereof."

Col. 292, line 57, in claim 4, "viva" should read --vivo--.

Col. 294, line 15, in claim 15, delete "any of".

Col. 294, line 17, in claim 16, delete "any of".

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, beginning with the text "<160> NUMBER OF SEQ ID NOS: 35" to and ending "<400> SEQUENCE: 35

Met	Pro	Thr	Trp	Ala	Trp	Trp	Leu	Phe	Leu	Val	Leu	Leu	Ala	Leu
1					5				10					15

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Washington, D.C. 20001-4413

Trp Ala Pro Ala Arg Gly"

20

in Col. 292 and insert the following Sequence Listing:

<160> NUMBER OF SEQ ID NOS: 45

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer useful to clone human growth hormone cDNA

<400> 1

cccaagaatt cccttatcca ggc

23

<210> 2

<211> 33

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<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer useful to clone human growth hormone cDNA

<400> 2

999aagctta gaagccacag gatccctcca cag

33

<210> 3

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 3

gataaagatt cccaac

16

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

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<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

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Garrett & Dunner, L.L.P.
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Washington, D.C. 20001-4413

9 2006

<400> 4
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17

<210> 5
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
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<222> 20)..(24)
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1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser
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<210> 8
<211> 21

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<212> DNA
<213> Artificial Sequence

<220>
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<223> synthetic oligonucleotide used to join DNA
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ac

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62

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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

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130	135	140	
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg 480			
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
145	150	155	160
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc 528			
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
	165	170	175
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg 576			
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
	180	185	190
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa 624			
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
	195	200	205
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc 672			
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
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aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa 720			
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
	225	230	235
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac 768			
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp			
	245	250	255
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc 816			
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
	260	265	270
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac 864			
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
	275	280	285
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca 912			
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
	290	295	300
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct 960			
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
	305	310	315
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga 1008			
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg			
	325	330	335
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca 1056			
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr			
	340	345	350
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa 1104			
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu			
	355	360	365

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro 370 375 380	1152
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu 385 390 395 400	1200
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro 405 410 415	1248
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys 420 425 430	1296
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys 435 440 445	1344
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His 450 455 460	1392
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser 465 470 475 480	1440
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr 485 490 495	1488
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp 500 505 510	1536
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala 515 520 525	1584
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu 530 535 540	1632
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys 545 550 555 560	1680
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val 565 570 575	1728
gct gca agt caa gct gcc tta ggc tta taacatctac attttaaagc atctcag Ala Ala Ser Gln Ala Ala Leu Gly Leu 580 585	1782

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<210> 18
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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
      35              40              45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
      50              55              60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
      65              70              75              80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
      85              90              95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
      100             105             110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
      115             120             125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
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Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
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Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
      165             170             175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
      180             185             190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
      195             200             205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
      210             215             220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
      225             230             235             240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
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Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
      260             265             270
  
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Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

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<210> 28

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

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<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

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<221> misc feature

<222> (38)

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MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

MAR 9 2006

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<221> signal
<223> signal peptide of natural human serum albumin protein

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<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
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Tyr Ser Arg Ser Leu Asp Lys Arg
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<210> 30
<211> 114
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<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

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<222> (75)..(81)
<223> XhoI restriction site

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<222> (98)..(114)
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<211> 43
<212> DNA
<213> Artificial Sequence

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<223> Stanniocalcin signal peptide

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  1             5             10             15

Ala

<210> 35
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  1             5             10             15

Trp Ala Pro Ala Arg Gly
          20

<210> 36
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<213> Homo sapiens

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aattcgaggg tgcaccgtca gtcttctctt tcccccaaaa acccaaggac accctcatga      120

tctcccgagc tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gacctgagg      180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg      240

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aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtag aagtgcaagg tctccaacaa agccctccca acccccatcg 360
agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcctc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgectgttc aaaggtctct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tcgacggct ccttcttctc ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag ggaacgtct tctcatgctc cgtgatgat gaggtctctc 660
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1 5

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<223> forward primer useful for generation of a synthetic gamma activation site
(GAS) containing promoter element

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cccgaaatat ctgccatctc aattag 86

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<210> 39
<211> 27
<212> DNA

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Washington, D.C. 20001-4413

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<213> Artificial Sequence

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27

<210> 40
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aaatatctgc catctcaatt agtcagcaac catagtcccc ccctaaactc cgcccatccc 120
gccctaactc cgcgccagtt cgcgccattc tccgcccat ggctgactaa ttttttttat 180
ttatgcagag gccgaggcgc cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
ttttggaggc ctaggctttt gcaaaaagct t 271

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<213> Artificial Sequence

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<223> primer useful for generation of a EGR/SEAP reporter construct

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<210> 42
<211> 31
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gcgaagcttc gcgactcccc ggateccgct c 31

<210> 43
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<213> Artificial Sequence

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<223> NF-KB binding site

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12

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ccatctcaat tag

73

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<223> Synthetic NF-KB/SV40 promoter

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cagttccgcc cattctccgc cccatggctg actaattttt ttatttatg cagaggccga 180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240

cttttgcaaa aagctt 256

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